sequences, respectively, said first and second hybridization complexes attached to first and second microspheres, respectively, randomly distributed on a surface of a substrate;

b) extending said first and second primers by the addition of a first nucleotide to the first detection position using a first enzyme to form first and second extended primers, respectively; and

c) detecting the release of pyrophosphate (PPi) to determine the type of said first nucleotide added onto said first and second primers, respectively.

2. (Amended) A method according to claim 1 wherein at least said first hybridization complex is covalently attached to said first microsphere.

3. (Amended) A method according to claim 1 wherein at least said first sequencing primer is attached to said first microsphere.

4. (Amended) A method according to claim 1 wherein said first and second hybridization complexes comprise said first and second target sequences, respectively, said first and second sequencing primers, respectively, and first and second capture probes, respectively, covalently attached to said first and second microspheres, respectively.

5. (Amended) A method according to claim 1 wherein said first and second hybridization complexes comprise said first and second target sequences, respectively, said first and second sequencing primers, a first and second adapter probe, respectively, and first and second capture probes, respectively, covalently attached to said first and second microspheres.

6. (Amended) A method according to claim 1 further comprising:
d) extending said first and second extended primers by the addition of a second nucleotide to the second detection position using said first enzyme; and
e) detecting the release of pyrophosphate (PPi) to determine the type of said second nucleotide added onto said first and second primers, respectively.

7. The method according to claim 1 wherein said PPi is detected by a method comprising:
a) contacting said PPi with a second enzyme that converts said PPi into ATP; and
b) detecting said ATP using a third enzyme.

8. A method according to claim 7 wherein said second enzyme is sulfurylase.

9. A method according to claim 7 wherein said third enzyme is luciferase.

10. (Amended) A method of sequencing a target nucleic acid comprising a first domain and an adjacent second domain, said second domain comprising a plurality of target positions, said method comprising:
a) providing a hybridization complex comprising said target sequence and a capture probe covalently attached to a microsphere randomly distributed on a surface of a substrate; and
b) determining the identity of a plurality of bases at said target positions.

11. A method according to claim 10 wherein said hybridization complex comprises said capture probe, an adapter probe, and said target sequence.

12. (Amended) A method according to claim 10 wherein said capture probe is a sequencing primer.

13. A method according to claim 10 wherein said determining comprises:
a) providing a sequencing primer hybridized to said second domain;
b) extending said primer by the addition of a first nucleotide to the first detection position using a first enzyme to form an extended primer;
c) detecting the release of pyrophosphate (PPi) to determine the type of said first nucleotide added onto said primer;
d) extending said primer by the addition of a second nucleotide to the second detection position using said enzyme; and
e) detecting the release of pyrophosphate (PPi) to determine the type of said first nucleotide added onto said primer.

14. The method according to claim 13 wherein said PPi is detected by a method comprising:
a) contacting said PPi with a second enzyme that converts said PPi into ATP; and
b) detecting said ATP using a third enzyme.

15. A method according to claim 14 wherein said second enzyme is sulfurylase.

16. A method according to claim 14 wherein said third enzyme is luciferase.

17. A method according to claim 10 wherein said determining comprises:
a) providing a sequencing primer hybridized to said second domain;
b) extending said primer by the addition of a first protected nucleotide using a

first enzyme to form an extended primer;

c) determining the identification of said first protected nucleotide;

d) removing the protection group;

e) adding a second protected nucleotide using said enzyme; and

f) determining the identification of said second protected nucleotide.

18. (Amended) A kit for nucleic acid sequencing comprising:

a) a composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres randomly distributed on said sites;

wherein said microspheres comprise capture probes;

b) an extension enzyme; and

c) dNTPs.

19. A kit according to claim 18 further comprising:

d) a second enzyme for the conversion of pyrophosphate (PPi) to ATP; and

e) a third enzyme for the detection of ATP.

20. A kit according to claim 18 wherein said dNTPs are labeled.

21. A kit according to claim 20 wherein each dNTP comprises a different label.

Please add the following new claims:

- -22. The method according to claim 1, wherein said substrate comprises discrete sites and said first and second microspheres are randomly distributed on said sites.